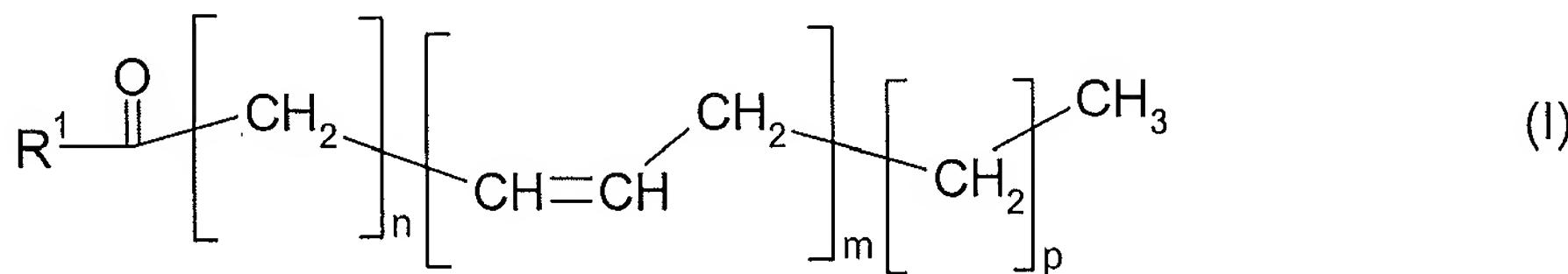


AMENDMENTS TO THE CLAIMS

Listing of Claims:

1. (Currently amended) A process for the production of compounds of the formula I

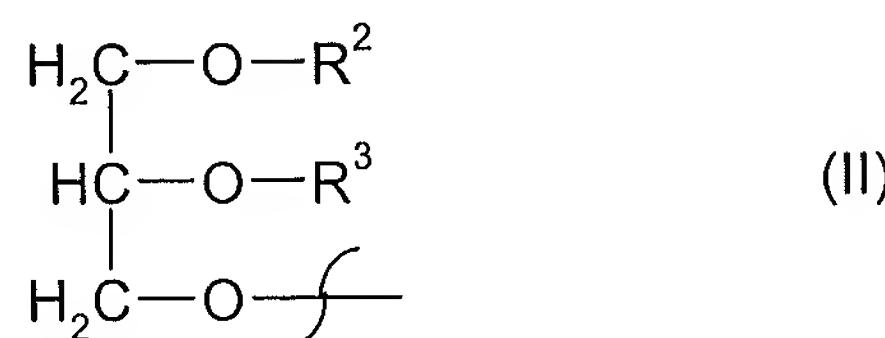


in a transgenic organism with a content of at least 1% by weight of these compounds based on the total lipid content of the transgenic organism, which comprises the following process steps:

- a) introducing, into the organism, at least one nucleic acid sequence which encodes a polypeptide with Δ6-desaturase activity, and
- b) introducing, into the organism, at least one nucleic acid sequence which encodes a polypeptide with Δ6-elongase activity, and
- c) introducing, into the organism, at least one nucleic acid sequence which encodes a polypeptide with Δ5-desaturase activity, and
- d) introducing, into the organism, at least one nucleic acid sequence which encodes a polypeptide with Δ5-elongase activity that elongates unsaturated C₂₀-fatty acids, and
- e) introducing, into the organism, at least one nucleic acid sequence which encodes a polypeptide with Δ4-desaturase activity, and

where the variables and substituents in formula I have the following meanings:

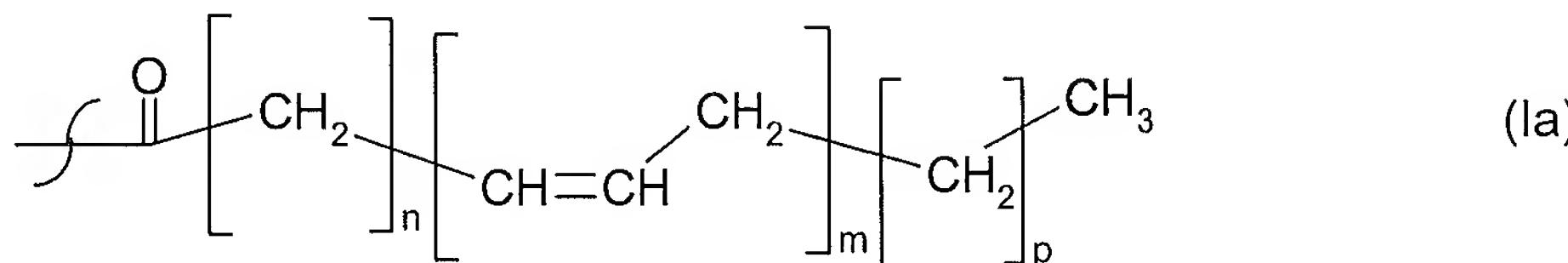
R¹ = hydroxyl, coenzyme A (thioester), lysophosphatidylcholine, lysophosphatidylethanolamine, lysophosphatidylglycerol, lysodiphosphatidylglycerol, lysophosphatidylserine, lysophosphatidylinositol, sphingo base or a radical of the formula II



in which

R^2 = hydrogen, lysophosphatidyl choline, lysophosphatidylethanolamine, lysophosphatidylglycerol, lysodiphosphatidylglycerol, lysophosphatidylserine, lysophosphatidylinositol or saturated or unsaturated C₂-C₂₄-alkylcarbonyl,

R^3 = hydrogen, saturated or unsaturated C₂-C₂₄-alkylcarbonyl, or R^2 and R^3 independently of one another are a radical of the formula Ia:



in which

n = 2, 3, 4, 5, 6, 7 or 9, m = 2, 3, 4, 5 or 6 and p = 0 or 3.

2. (Previously presented) The process according to claim 1, wherein the at least one nucleic acid sequence which encodes a polypeptide with $\Delta 6$ -desaturase, $\Delta 6$ -elongase, $\Delta 5$ -desaturase, $\Delta 5$ -elongase or $\Delta 4$ -desaturase activity is selected from the group consisting of:

- a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137 or SEQ ID NO: 183, or

- b) a nucleic acid sequence which, as the result of the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO: 6, SEQ ID NO: 8,

SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138 or SEQ ID NO: 184, and

c) a derivative of the nucleic acid sequence shown in SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137 or SEQ ID NO: 183 which encodes a polypeptide with at least 40% identity at the amino acid level with SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80,

SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138 or SEQ ID NO: 184 and having Δ 6-desaturase, Δ 6-elongase, Δ 5-desaturase, Δ 5-elongase or Δ 4-desaturase activity.

3. (Previously presented) The process according to claim 1, wherein a nucleic acid sequence which encodes a polypeptide with ω 3-desaturase activity is additionally introduced into the organism, wherein said nucleic acid sequence is selected from the group consisting of:

- a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 87 or SEQ ID NO: 105,
- b) a nucleic acid sequence which, as the result of the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO: 88 or SEQ ID NO: 106, and
- c) a derivative of the nucleic acid sequence shown in SEQ ID NO: 87 or SEQ ID NO: 105 which encodes a polypeptide with at least 70% identity at the amino acid level with SEQ ID NO: 88 or SEQ ID NO: 106 and having ω 3-desaturase activity.

4. (Currently amended) The process according to claim 1, wherein a nucleic acid sequence which encodes a polypeptide with Δ 12-desaturase activity is additionally introduced into the organism, wherein said nucleic acid sequence is selected from the group consisting of:

- a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 107 or SEQ ID NO: 109,
- b) a nucleic acid sequence which, as the result of the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO: 108 or SEQ ID NO: 110, and
- c) a derivative of the nucleic acid sequence shown in SEQ ID NO: 107 or SEQ ID NO: 110 109 which encodes a polypeptide with at least 70% identity at the amino acid level with SEQ ID NO: 108 or SEQ ID NO: 110 and having Δ 12-desaturase activity.

5. (Previously presented) The process according to claim 1, wherein the substituents R² or R³ independently of one another are saturated or unsaturated C₁₈-C₂₂-alkylcarbonyl.

6. (Previously presented) The process according to claim 1, wherein the substituents R² or R³ independently of one another are unsaturated C₁₈-, C₂₀- or C₂₂-alkylcarbonyl with at least two double bonds.
7. (Previously presented) The process according to claim 1, wherein the transgenic organism is a transgenic microorganism or a transgenic plant.
8. (Previously presented) The process according to claim 1, wherein the transgenic organism is an oil-producing plant, a vegetable plant or an ornamental.
9. (Previously presented) The process according to any of claim 1, wherein the transgenic organism is a transgenic plant selected from the group consisting of the plant families: Adelotheciaceae, Anacardiaceae, Asteraceae, Apiaceae, Betulaceae, Boraginaceae, Brassicaceae, Bromeliaceae, Caricaceae, Cannabaceae, Convolvulaceae, Chenopodiaceae, Cryptecodiniaceae, Cucurbitaceae, Ditrichaceae, Elaeagnaceae, Ericaceae, Euphorbiaceae, Fabaceae, Geraniaceae, Gramineae, Juglandaceae, Lauraceae, Leguminosae, Linaceae and Prasinophyceae.
10. (Previously presented) The process according to claim 1, wherein the compounds of the formula I are isolated from the organism in the form of oils, lipids or free fatty acids.
11. (Previously presented) The process according to claim 1, wherein the compounds of the formula I are isolated in a concentration of at least 5% by weight based on the total lipid content of the transgenic organism.
- 12-34. (Cancelled)
35. (New) The process of claim 1, wherein the polypeptide with Δ5-elongase activity elongates only unsaturated C₂₀-fatty acids.